



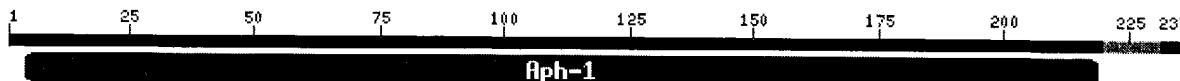
## NCBI Conserved Domain Search

[New Search](#)[PubMed](#)[Nucleotide](#)[Protein](#)[Structure](#)[CDD](#)[Taxonomy](#)[Help?](#)**RPS-BLAST 2.2.9 [May-01-2004]**

**Query=** local sequence:  
(237 letters)

**Database:** cdd.v2.00  
11,382 PSSMs; 2,824,437 total columns

Click on boxes for multiple alignments



Show  Domain Relatives

PSSMs producing significant alignments:

Score E  
(bits) value

gnl|CDD|26475 pfam06105, Aph-1, Aph-1 protein. This family consists of sever... 191 6e-50

gnl|CDD|26475, pfam06105, Aph-1, Aph-1 protein. This family consists of several eukaryotic Aph-1 proteins. Gamma-secretase catalyses the intramembrane proteolysis of Notch, beta-amyloid precursor protein, and other substrates as part of a new signaling paradigm and as a key step in the pathogenesis of Alzheimer's disease. It is thought that the presenilin heterodimer comprises the catalytic site and that a highly glycosylated form of nicastrin associates with it. Aph-1 and Pen-2, two membrane proteins genetically linked to gamma-secretase, associate directly with presenilin and nicastrin in the active protease complex. Co-expression of all four proteins leads to marked increases in presenilin heterodimers, full glycosylation of nicastrin, and enhanced gamma-secretase activity.

CD-Length = 246 residues, 95.1% aligned  
Score = 191 bits (487), Expect = 6e-50

Query: 4	VFFGCAFIAGFP--MMYVFTIAEEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD	59
Sbjct: 5	VFFGCTFIAFGPSLALFVSTIARDPLRIIILIAGAFFWLVSLLSSLVWFILVPLTDKAD	64
Query: 60	GPTQKYLLIFGAWSWI--QEMF--AYYKLLK-MSEGLKSINPGETAPSMLRM--YVSGLG	112
Sbjct: 65	AWWQYGLLIFGVVSVCFQELFRFAYYKLLKAEEGLDSIAEDGRRPISKQLAYVSGLG	124
Query: 113	FGIMSGVFSM--TLSDSLGPVTGVIHGDSQFFLYSA-GTLVIIILLHVFWGIVFFDGCEM	169
Sbjct: 125	FGIISGVFSVNVILADALGPVTGVIHGDSKLFLLTSAFMALAIIILLHTFWGVVFFDACEK	184
Query: 170	--KKGILLIALTHLLVSAQTFIISYYGINLM-AFIILVV-GTWAFIAAGGSCRS	219
Sbjct: 185	NNYIALGIVPVSHLLVSMLTFLNPAYEGSLVPLYLVLSLMGVWAFVVAGGSLRS	238

**Citing CD-Search:** Marchler-Bauer A, Anderson JB, DeWeese-Scott C, Fedorova ND, Geer LY, He S,

Hurwitz DI, Jackson JD, Jacobs AR, Lanczycki CJ, Liebert CA, Liu C, Madej T, Marchler GH, Mazumder R, Nikolskaya AN, Panchenko AR, Rao BS, Shoemaker BA, Simonyan V, Song JS, Thiessen PA, Vasudevan S, Wang Y, Yamashita RA, Yin JJ, and Bryant SH (2003), "CDD: a curated Entrez database of conserved domain alignments", **Nucleic Acids Res.** **31**:383-387.

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# results of BLAST

BLASTP 2.2.9 [May-01-2004]

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1087209714-1737-5403932422.BLASTQ4

**Query=**

(237 letters)

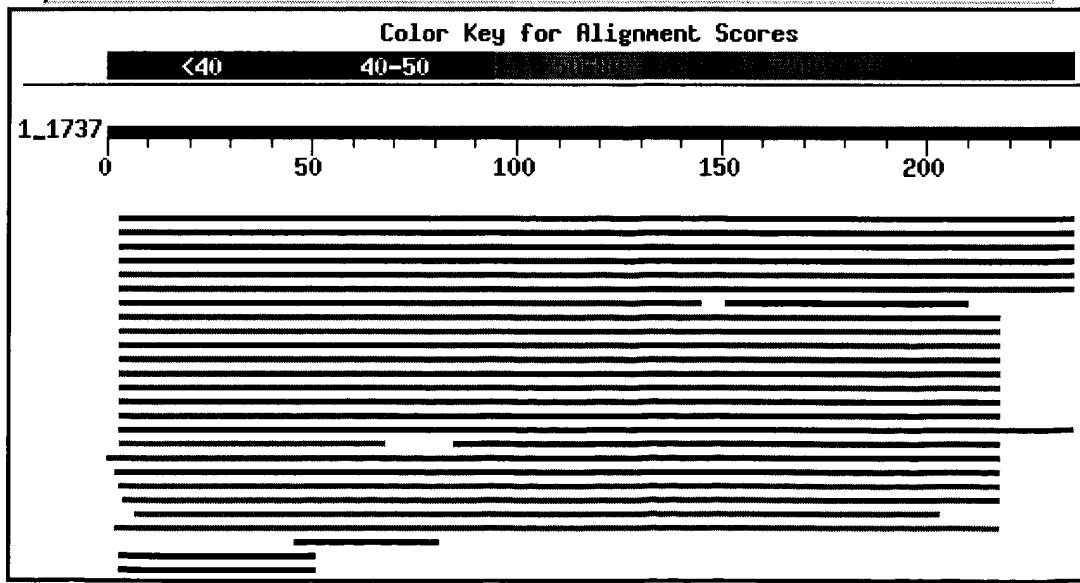
**Database:** All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples  
1,860,402 sequences; 617,572,895 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

## Distribution of 28 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



gi 18088649 gb AAH20905.1	Presenilin stabilization factor-like [Homo sapiens]	283	3e-75	L
gi 13775224 ref NP_112591.1	presenilin stabilization factor-like [Homo sapiens]	281	8e-75	L
gi 37182518 gb AAQ89061.1	TAAV688 [Homo sapiens]	281	8e-75	
gi 29243936 ref NP_808251.1	hypothetical protein 4632417K0...	247	2e-64	L
gi 34864291 ref XP_217185.2	similar to RIKEN cDNA 0610008A...	240	2e-62	L
gi 21492616 ref NP_080950.1	RIKEN cDNA 0610008A10 [Mus mus...	233	2e-60	L
gi 26324468 dbj BAC25988.1	unnamed protein product [Mus mu...	186	5e-46	L
gi 37077149 sp Q8BVF7 AP1A_MOUSE	Gamma-secretase subunit AP...	176	2e-43	L
gi 12654775 gb AAH01230.1	APH-1A protein [Homo sapiens]	176	3e-43	L
gi 37077707 sp Q96BI3 AP1A_HUMAN	Gamma-secretase subunit AP...	176	3e-43	L
gi 34858248 ref XP_345252.1	similar to Aphla-pending prote...	176	3e-43	L
gi 7705787 ref NP_057106.1	CGI-78 protein [Homo sapiens] >...	173	3e-42	L
gi 22203751 ref NP_666216.1	anterior pharynx defective 1A ...	172	5e-42	L
gi 14250557 gb AAH08732.1	APH-1A protein [Homo sapiens] >g...	172	6e-42	L
gi 41056229 ref NP_956409.1	anterior pharynx defective 1B ...	171	1e-41	L
gi 34864287 ref XP_343418.1	similar to RIKEN cDNA 0610008A...	171	1e-41	L
gi 26347159 dbj BAC37228.1	unnamed protein product [Mus mu...	120	2e-26	L
gi 31233667 ref XP_318923.1	ENSANGP00000015809 [Anopheles ...	117	2e-25	
gi 47214485 emb CAG12490.1	unnamed protein product [Tetrao...	116	4e-25	
gi 48095709 ref XP_392345.1	similar to CG2855-PA [Apis mel...	116	5e-25	L
gi 20129183 ref NP_608710.1	CG2855-PA [Drosophila melanoga...	105	1e-21	L
gi 39580694 emb CAE70374.1	Hypothetical protein CBG16933 [...]	64	2e-09	
gi 20829201 ref XP_129583.1	similar to CGI-78 protein [Mus...]	57	4e-07	
gi 17509423 ref NP_492469.1	i-78 protein like, Anterior PH...	52	1e-05	L
gi 48129682 ref XP_393309.1	similar to Na/Ca exchange prot...	33	5.3	L
gi 48103053 ref XP_395490.1	similar to CG5880-PA [Apis mel...	32	7.6	
gi 16763476 ref NP_459091.1	glutathione-regulated K <sup>+</sup> efflu...	32	9.6	
gi 16759081 ref NP_454698.1	glutathione-regulated potassiu...	32	9.6	

## Alignments

[Get selected sequences](#)  [Select all](#)  [Deselect all](#)

>gi|18088649|gb|AAH20905.1| L Presenilin stabilization factor-like [Homo sapiens]  
Length = 257

Score = 283 bits (723), Expect = 3e-75

Identities = 202/253 (79%), Positives = 211/253 (83%), Gaps = 19/253 (7%)

Query: 4 VFFGCAFIAGPMM--YVFTIAEPLRIIFLIAAGAFN-LVSLISSL-WFMARVTIDNKD 59  
VFFGCAFIAGP + YVFTIA EPLRIIFLIAAGAF LVSLISSL WFMARV IDNKD

Sbjct: 5 VFFGCAFIAGP~~ALALYVFTIATEPLRIIFLIAAGAFF~~WLVSLISSLVWFMARVIIDNKD 64

Query: 60 GPTQKYLLIFGAWS--WIQEMF--AYYKLLK-MSEG~~LKSINPGETAPS~~MRLM-YVSGLG~~F~~ 113  
GPTQKYLLIFGA+ +IQEMF AYYKLLK SEGLKSINPGETAPS~~MRL~~+ YVSGLG~~F~~

Sbjct: 65 GPTQKYLLIFGA~~F~~VSVYI~~QEMFR~~AYYKLLK~~A~~SEG~~LKSINPGETAPS~~MRLAYVSGLG~~F~~ 124

Query: 114 GIMSGVFSM--TLSDSLGP~~G~~TVGIHGDS~~P~~QFFLYSA-GTLV~~II~~LLHVFWGIVFFDGCE-M 169  
GIMSGVFS TLSDSLGP~~G~~TVGIHGDS~~P~~QFFLYSA TLV~~II~~LLHVFWGIVFFDGCE

Sbjct: 125 GIMSGVFSFVNTLSDSLGP~~G~~TVGIHGDS~~P~~QFFLYSA~~F~~MTLV~~II~~LLHVFWGIVFFDGCEKK 184

Query: 170 KWG-ILLIALTHLLVSAQTFISSIONYGINLM-AFIILVV-GTWAFIAAGGSCRS--XXXXX 224  
 KWG +L++ LTHLLVSAQTFISSIONYGINL AFIILV+ GTWAF+AAGGSCRS  
 Sbjct: 185 KWGILLIVLLTHLLVSAQTFISSIONYGINLASAFIILVLMGTWAFLAAGGSCRSLKLCLLC 244

Query: 225 XXXXXXXYNQSR 237  
 YNQSR  
 Sbjct: 245 QDKNFLLYNQSR 257

[>gi|13775224|ref|NP\_112591.1| L presenilin stabilization factor-like [Homo sapiie  
 gi|37077447|sp|Q8WW43|AP1B\_HUMAN L Gamma-secretase subunit APH-1B (APH-1b) (Aph-1  
 stabilization factor-like)  
 gi|12052866|emb|CAB66606.1| L hypothetical protein [Homo sapiens]  
 gi|24637564|gb|AAN63817.1| L presenilin stabilization factor-like protein [Homo s  
 Length = 257

Score = 281 bits (719), Expect = 8e-75  
 Identities = 201/253 (79%), Positives = 211/253 (83%), Gaps = 19/253 (7%)

Query: 4 VFFGCAFIAGPMM--YVFTIAEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGCAFIAGP + YVFTIA EPLRIIFLIAGAF LVSLLISSL WFMARV IDNKD  
 Sbjct: 5 VFFGCAFIAGPALALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKD 64

Query: 60 GPTQKYLLIFGAWS--WIQEMF--AYYKLLK-MSEGLKSINPGETAPSMRLM-YVSGLGF 113  
 GPTQKYLLIFGA+ +I+EMF AYYKLLK SEGLKSINPGETAPSMRL+ YVSGLGF  
 Sbjct: 65 GPTQKYLLIFGAFFVSVYIREMFRFAYYKLLKASEGLKSINPGETAPSMRLAYVSGLGF 124

Query: 114 GIMSGVFSM--TLSDSLGP GTVGIHGDS PQFFLYSA-GTLVIIILLHVFWGIVFFDGCE-M 169  
 GIMSGVFS TLSDSLGP GTVGIHGDS PQFFLYSA TLVIIILLHVFWGIVFFDGCE  
 Sbjct: 125 GIMSGVFSVNTLSDSLGP GTVGIHGDS PQFFLYSAFMTLVIILLHVFWGIVFFDGCEKK 184

Query: 170 KWG-ILLIALTHLLVSAQTFISSIONYGINLM-AFIILVV-GTWAFIAAGGSCRS--XXXXX 224  
 KWG +L++ LTHLLVSAQTFISSIONYGINL AFIILV+ GTWAF+AAGGSCRS  
 Sbjct: 185 KWGILLIVLLTHLLVSAQTFISSIONYGINLASAFIILVLMGTWAFLAAGGSCRSLKLCLLC 244

Query: 225 XXXXXXXYNQSR 237  
 YNQSR  
 Sbjct: 245 QDKNFLLYNQSR 257

[>gi|37182518|gb|AAQ89061.1| TAAV688 [Homo sapiens]  
 Length = 257

Score = 281 bits (719), Expect = 8e-75  
 Identities = 202/253 (79%), Positives = 211/253 (83%), Gaps = 19/253 (7%)

Query: 4 VFFGCAFIAGPMM--YVFTIAEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGCAFIAGP + YVFTIA EPLRIIFLIAGAF LVSLLISSL WFMARV IDNKD  
 Sbjct: 5 VFFGCAFIAGPALALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKD 64

Query: 60 GPTQKYLLIFGAWS--WIQEMF--AYYKLLK-MSEGLKSINPGETAPSMRLM-YVSGLGF 113  
 GPTQKYLLIFGA+ +I+EMF AYYKLLK SEGLKSINPGETAPSMRL+ YVSGLGF  
 Sbjct: 65 GPTQKYLLIFGAFFVSVYI QEMFRFAYYKLLKASEGLKSINPGETAPSMRLAYVSGLGF 124

Query: 114 GIMSGVFSM--TLSDSLGP GTVGIHGDS PQFFLYSA-GTLVIIILLHVFWGIVFFDGCE-M 169

GIMSGVFS TLSDSLPGTVGIHGDSQFFLYSA TLVIIILLHVFWGIVFFDGCE  
 Sbjct: 125 GIMSGVFSFVNTLSLDSLPGTVGIHGDSQFFLYSAFMTLVIIILLHVFWGIVFFDGCEKK 184

Query: 170 KWG-ILLIALTHLLVSAQTFISSIONYGINLM-AFIILVV-GTWAFIAAGGSCRS--XXXXX 224  
 KWG +L++ LTHLLVSAQTFISSIONYGINL AFIILV+ GTWAF+AAGGSCRS  
 Sbjct: 185 KWGILLIVLLTHLLVSAQTFISSIONYGINLASAFIILVLMGTWAFLAAGGCRSLKLCLLC 244

Query: 225 XXXXXXXYNQSR 237  
 YNQSR  
 Sbjct: 245 QDKNFLLYNQSR 257

>gi|29243936|ref|NP\_808251.1| L hypothetical protein 4632417K02 [Mus musculus]  
 gi|37077156|sp|Q8C7N7|AP1B\_MOUSE Gamma-secretase subunit APH-1B  
 gi|26340556|dbj|BAC33940.1| L unnamed protein product [Mus musculus]  
 Length = 257

Score = 247 bits (630), Expect = 2e-64  
 Identities = 173/253 (68%), Positives = 195/253 (77%), Gaps = 19/253 (7%)

Query: 4 VFFGCAFIAGPMM--YVFTIAEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGCAFIAGP + YVFTIA +PLR+IIFIAGAF LVSLL+SS+ WF+ RV DN+D  
 Sbjct: 5 VFFGCAFIAGPALALYVFTIATDPLRVIIFIAGAFFWLVSLLLSSVFWFLVRVITDNRD 64

Query: 60 GPTQKYLLIFGAW--SWIQEMF--AYYKLLK-MSEGLKSINPGETAPSMRLM-YVSGLGF 113  
 GP Q YLLIFG IQE+F AYYKLLK SEGLKSINP ETAPSMRL+ YVSGLGF  
 Sbjct: 65 GPVQNYLLIFGVLLSVCIQELFRLAYYKLLKKASEGLKSINPEETAPSMRLAYVSGLGF 124

Query: 114 GIMSGVFSM--TLSDSLPGTVGIHGDSQFFLYSA-GTLVIIILLHVFWGIVFFDGCEM- 169  
 GIMSGVFS TLS+SLPGTVGIHGDSQFFL SA TLV+I+LHVFWG+VFFDGCE  
 Sbjct: 125 GIMSGVFSFVNLSLDSLPGTVGIHGDSQFFLNSAFMTLVVIMLHVFWGVVFFDGCEKN 184

Query: 170 KW-GILLIALTHLLVSAQTFISSIONYGINLM-AFIILVV-GTWAFIAAGGSCRS--XXXXX 224  
 KW +L + LTHL+VS QTF+S YY +NL+ A+II+V+ G WAF AGGSCRS  
 Sbjct: 185 KWYTLTLLTHLLVSVTQFLSPYYEVNLVTAYIIMVLMGIWAFYVAGGCRSLKLCLLC 244

Query: 225 XXXXXXXYNQSR 237  
 YNQSR  
 Sbjct: 245 QDKDFLLYNQSR 257

>gi|34864291|ref|XP\_217185.2| L similar to RIKEN cDNA 0610008A10 [Rattus norvegi  
 Length = 257

Score = 240 bits (612), Expect = 2e-62  
 Identities = 171/253 (67%), Positives = 193/253 (76%), Gaps = 19/253 (7%)

Query: 4 VFFGCAFIAGPMM--YVFTIAEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGCAFIAGP + Y+FTIA +PLR+IIFIAGAF LVSLL+SS+ WF+ RV DN+D  
 Sbjct: 5 VFFGCAFIAGPALALYLTIATDPLRVIIFIAGAFFWLVSLLLSSVFWFLVRVITDNRD 64

Query: 60 GPTQKYLLIFGAW--SWIQEMF--AYYKLLK-MSEGLKSINPGETAPSMRLM-YVSGLGF 113  
 GP Q YLLIFG IQE+F AYY+LLK SEGLKSINP ETAPSMRL+ YVSGLGF  
 Sbjct: 65 GPVQNYLLIFGVLLSVCIQELFRLAYYRLLKKASEGLKSINPEETAPSMRLAYVSGLGF 124

Query: 114 GIMSGVFSM--TLSDSLPGTVGIHGDSQFFLYSA-GTLVIIILLHVFWGIVFFDGCEM- 169  
 GIMSGVFS TLS++LPGTVGIHGDSQFFL SA TLVII+LHVFWGIVFFDGCE

Sbjct: 125 GIMSGVFSVNTLSNALGP GTVGIHGDSPQFFLNSAFMTLVIIMLHVFWGIVFFDGCEKN 184

Query: 170 KWGI-LLIALTHLLVSAQTFISSIONYGINLM-AFIILVV-GTWAFIAAGGSCRS--XXXXX 224  
KW I L + LTHLLVS QT +S +Y +NL+ A+II+V+ G WAF AGGS RS

Sbjct: 185 KKYILLTVLLTHLLVSTQTLLSPHYEVNLVTAYIIMVLMGIWAFCVAGGSRRSLKLCLLC 244

Query: 225 XXXXXXXYQRSR 237  
YNQRSR

Sbjct: 245 QDKDFLLYNQRSR 257

► >gi|21492616|ref|NP\_080950.1| L RIKEN cDNA 0610008A10 [Mus musculus]  
gi|37077773|sp|Q9DCZ9|AP1C\_MOUSE L Putative gamma-secretase subunit APH-1C  
gi|12832198|dbj|BAB22004.1| L unnamed protein product [Mus musculus]  
gi|29747906|gb|AAH50923.1| L RIKEN cDNA 0610008A10 [Mus musculus]  
gi|38648719|gb|AAH63254.1| L RIKEN cDNA 0610008A10 [Mus musculus]  
Length = 258

Score = 233 bits (594), Expect = 2e-60  
Identities = 169/254 (66%), Positives = 193/254 (75%), Gaps = 20/254 (7%)

Query: 4 VFFGCAFIAGP--MYVFTIAEEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
VFFGCAFIAGP +Y+FTIA +PLR+IFLIAGAF LVSL+SS+ WF+ RV +N+D  
Sbjct: 5 VFFGCAFIAGPAFALYLFTIATDPLRVIFLIAGAFFWLVSLLSSMFWFVFLVRVITNNRD 64

Query: 60 GPTQKYLLIFGAW--SWIQEMF--AYYKLLK-MSEGLKSINPGE-TAPSMRLM-YVSGLG 112  
Q YLLIFGA IQE+F AYYKLLK SEGLKSINP E APSMRL+ YVSGLG  
Sbjct: 65 ESVQNYLLIFGALLSVCIQELFRLAYYKLLKASEGLKSINPEEDIAPSMRLLAYVSGLG 124

Query: 113 FGIMSGVFSM--TLSDSLGP GTVGIHGDSPQFFLYSA-GTLVIIILLHVFWGIVFFDGCEM 169  
FGIMSGVFS TLS+SLGP GTVGIHGDSPQFFL SA TLV+I+LHVFWG+VFFDGCE  
Sbjct: 125 FGIMSGVFSVNTLSNLGP GTVGIHGDSPQFFLNSAFMTL VVIMLHVFWGVVFFDGCEK 184

Query: 170 -KW-GILLIALTHLLVSAQTFISSIONYGINLM-AFIILVV-GTWAFIAAGGSCRS--XXXX 223  
KW +L + LTHL+VS QT+S YY +NL+ A+II+V+ G WAF AGGSCRS  
Sbjct: 185 NKWYTLLTVLLTHLVVSTQTFLSPYYEVNLVTAYIIMVLMGIWAFYVAGGSCRS LKFCLL 244

Query: 224 XXXXXXXXQRSR 237  
YNQRSR

Sbjct: 245 CQDKDFLLYNQRSR 258

► >gi|26324468|dbj|BAC25988.1| L unnamed protein product [Mus musculus]  
Length = 212

Score = 186 bits (471), Expect = 5e-46  
Identities = 117/155 (75%), Positives = 127/155 (81%), Gaps = 12/155 (7%)

Query: 4 VFFGCAFIAGPMM--YVFTIAEEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
VFFGCAFIAGP + YVFTIA +PLR+IFLIAGAF LVSL+SS+ WF+ RV DN+D  
Sbjct: 5 VFFGCAFIAGPAFALYLFTIATDPLRVIFLIAGAFFWLVSLLSSVFWFLVRVITDNRD 64

Query: 60 GPTQKYLLIFGAW--SWIQEMF--AYYKLLK-MSEGLKSINPGETAPSMRLM-YVSGLG 113  
GP Q YLLIFG IQE+F AYYKLLK SEGLKSINP ETAPSMRL+ YVSGLG  
Sbjct: 65 GPVQNYLLIFGVLLSVCIQELFRLAYYKLLKASEGLKSINPEETAPSMRLLAYVSGLG 124

Query: 114 GIMSGVFSM--TLSDSLGP GTVGIHGDSPQFFLYS 146  
 GIMSGVFS TLS+SLGP GTVGIHGDSPQFFL S  
 Sbjct: 125 GIMSGVFSFVN TLSNSLGP GTVGIHGDSPQFFLNS 159

□>gi|37077149|sp|Q8BVF7|AP1A\_MOUSE L Gamma-secretase subunit APH-1A  
gi|18848275|gb|AAH24111.1| L 6530402N02Rik protein [Mus musculus]  
 Length = 265

Score = 176 bits (447), Expect = 2e-43  
 Identities = 124/234 (52%), Positives = 159/234 (67%), Gaps = 18/234 (7%)

Query: 4 VFFGCAFIAGP M--MYVFTIAEPLRIIFL IAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGC F+AFGP +++ T+A +PLR+I L+AGAF LVSLL++S+ WF+ D D  
 Sbjct: 5 VFFGCTFVAFGP AFSLFLITVAGDPLRVII ILVAGAFFWLVSLLL ASVVWFILVHVTDRSD 64

Query: 60 GPTQKYLLIFGAWS--WIQEMF--AYYKLLKMS-EGLKSINPGETAP-SMRLM-YVSGLG 112  
 Q LLIFGA +QE+F AYYKLLK + EGL S++ +P S+R M YVSGL  
 Sbjct: 65 ARLQYGLLIFGA AVS VLLQEVFRFAYYKLLKADEGLASLSEDGRSPISIRQ MAYVSGLS 124

Query: 113 FGIMSGVFSM T--LSDSLGP GTVGIHGDSPQFFLYSAG-TLVI ILLHV FWGIVFFDGCEM 169  
 FGI+SGVFS+ L+D+LGPG VGIHGDSP +FL SA T IILLH FWG+VFFD CE  
 Sbjct: 125 FGIISGVFSV NI LADALGP GVVG I HGDSP YYFL T SAFL TAAI ILLH FWGVV FF D A C E R 184

Query: 170 K--WGILLI ALTHLLVSAQTFI SYYG I N LMAFI I L VV--GTWAFIAAGGSCRS 219  
 + W + L+ +HLL S TF++ +Y +L+ + V G WAFI AGGS RS  
 Sbjct: 185 RRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRS 238

□>gi|12654775|gb|AAH01230.1| L APH-1A protein [Homo sapiens]  
 Length = 265

Score = 176 bits (447), Expect = 3e-43  
 Identities = 124/234 (52%), Positives = 159/234 (67%), Gaps = 18/234 (7%)

Query: 4 VFFGCAFIAGP M--MYVFTIAEPLRIIFL IAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGC F+AFGP +++ T+A +PLR+I L+AGAF LVSLL++S+ WF+ D D  
 Sbjct: 5 VFFGCTFVAFGP AFAFLITVAGDPLRVII ILVAGAFFWLVSLLL ASVVWFILVHVTDRSD 64

Query: 60 GPTQKYLLIFGAWS--WIQEMF--AYYKLLKMS-EGLKSINPGETAP-SMRLM-YVSGLG 112  
 Q LLIFGA +QE+F AYYKLLK + EGL S++ +P S+R M YVSGL  
 Sbjct: 65 ARLQYGLLIFGA AVS VLLQEVFRFAYYKLLKADEGLASLSEDGRSPISIRQ MAYVSGLS 124

Query: 113 FGIMSGVFSM T--LSDSLGP GTVGIHGDSPQFFLYSAG-TLVI ILLHV FWGIVFFDGCEM 169  
 FGI+SGVFS+ L+D+LGPG VGIHGDSP +FL SA T IILLH FWG+VFFD CE  
 Sbjct: 125 FGIISGVFSV NI LADALGP GVVG I HGDSP YYFL T SAFL TAAI ILLH FWGVV FF D A C E R 184

Query: 170 K--WGILLI ALTHLLVSAQTFI SYYG I N LMAFI I L VV--GTWAFIAAGGSCRS 219  
 + W + L+ +HLL S TF++ +Y +L+ + V G WAFI AGGS RS  
 Sbjct: 185 RRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSIRS 238

□>gi|37077707|sp|Q96B13|AP1A\_HUMAN Gamma-secretase subunit APH-1A (APH-1a) (Aph-1  
 stabilization factor) (CGI-78) (UNQ579/PRO1141)  
gi|15990414|gb|AAH15568.1| L APH-1A protein [Homo sapiens]

gi|18088501|gb|AAH20590.1| L APH-1A protein [Homo sapiens]  
 gi|25989510|gb|AAM61956.1| presenilin stabilization factor b [Homo sapiens]  
 Length = 265

Score = 176 bits (447), Expect = 3e-43  
 Identities = 124/234 (52%), Positives = 159/234 (67%), Gaps = 18/234 (7%)

Query: 4 VFFGCAFIAGPMP--MYVFTIAEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGC F+AFGP +++ T+A +PLR+I L+AGAF LVSLL++S+ WF+ D D  
 Sbjct: 5 VFFGCTFVAFGPAFALFLITVAGDPLRVIIILVAGAFFWLVSSLASVWVWFLVHVTDRSD 64

Query: 60 GPTQKYLLIFGAWS--WIQEMF--AYYKLLKMS-EGLKSINPGETAP-SMRLM-YVSGLG 112  
 Q LLIFGA +QE+F AYYKLLK + EGL S++ +P S+R M YVSGL  
 Sbjct: 65 ARLQYGLLIFGAAVSVLQEVFRFAYYKLLKADEGLASLSEDGRSPISIRQMAVSGLS 124

Query: 113 FGIMSGVFSMT--LSDSLGPGTVGIHGDSQFFLYSAG-TLVIILLHVFWGIVFFDGCEM 169  
 FGI+SGVFS+ L+D+LGPG VGIHGDS +FL SA T IILLH FWG+VFFD CE  
 Sbjct: 125 FGIISGVFSVINILADALGPGVVGHIHGDSYYFLTS AFLTAAIILLHTFWGVVFFDACER 184

Query: 170 K--WGILLIALTHLLVSAQTFIISYYGINLMAFIILVV--GTWAFIAAGGSCRS 219  
 + W + L+ +HLL S TF++ +Y +L+ + V G WAFI AGGS RS  
 Sbjct: 185 RRYWALGLVVGSLLTSGLTFLNPWYEASLLPIYAVTWSMGLWAFITAGGSLRS 238

gi|34858248|ref|XP\_345252.1| L similar to Aphla-pending protein [Rattus norvegicus]  
 Length = 265

Score = 176 bits (446), Expect = 3e-43  
 Identities = 123/234 (52%), Positives = 159/234 (67%), Gaps = 18/234 (7%)

Query: 4 VFFGCAFIAGPMP--MYVFTIAEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGC F+AFGP +++ T+A +PLR+I L+AGAF LVSLL++S+ WF+ D D  
 Sbjct: 5 VFFGCTFVAFGPAFALFLITVAGDPLRVIIILVAGAFFWLVSSLASVWVWFLVHVTDRSD 64

Query: 60 GPTQKYLLIFGAWS--WIQEMF--AYYKLLKMS-EGLKSINPGETAP-SMRLM-YVSGLG 112  
 Q LLIFGA +QE+F AYYKLLK + EGL S++ +P S+R M YVSGL  
 Sbjct: 65 ARLQYGLLIFGAAVSVLQEVFRFAYYKLLKADEGLASLSEDGRSPISIRQMAVSGLS 124

Query: 113 FGIMSGVFSMT--LSDSLGPGTVGIHGDSQFFLYSAG-TLVIILLHVFWGIVFFDGCEM 169  
 FGI+SGVFS+ L+D+LGPG VGIHGDS +FL SA T IILLH FWG+VFFD CE  
 Sbjct: 125 FGIISGVFSVINILADALGPGVVGHIHGDSYYFLTS AFLTAAIILLHTFWGVVFFDACER 184

Query: 170 K--WGILLIALTHLLVSAQTFIISYYGINLMAFIILVV--GTWAFIAAGGSCRS 219  
 + W + L+ +HLL S TF++ +Y +L+ + V G WAF+ AGGS RS  
 Sbjct: 185 RRYWALGLVVGSLLTSGLTFLNPWYEASLLPIYAVTWSMGLWAFITAGGSLRS 238

gi|7705787|ref|NP\_057106.1| L CGI-78 protein [Homo sapiens]  
 gi|4929623|gb|AAD34072.1| L CGI-78 protein [Homo sapiens]  
 gi|24637562|gb|AAN63816.1| L presenilin stabilization factor [Homo sapiens]  
 Length = 251

Score = 173 bits (438), Expect = 3e-42  
 Identities = 124/234 (52%), Positives = 159/234 (67%), Gaps = 18/234 (7%)

Query: 4 VFFGCAFIAGPMP--MYVFTIAEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59

VFFGC F+AFGP    +++ T+A +PLR+I L+AGAF    LVSLL++S+ WF+    D D  
 Sbjct: 5    VFFGCTFVAFGPAFALFLITVAGDPLRVIIILVAGAFFWLVSSLASVVWFILVHVTDRSD 64

Query: 60    GPTQKYLLIFGAWS--WIQEMF--AYYKLLKMS-EGLKSINPGETAP-SMRLM-YVSGLG 112  
 Q    LLIFGA    +QE+F    AYYKLLK + EGL S++    +P S+R M YVSGL  
 Sbjct: 65    ARLQYGLLIFGAAVSVLQEVFRFAYYKLLKADEGLASLSEDGRSPISIRQMAVSGLS 124

Query: 113    FGIMSGVFSMT--LSDSLGPGTVGIHGDSQFFLYSAG-TLVIILLHVFWGIVFFDGCEM 169  
 FGI+SGVFS+    L+D+LGPG    VGIHGDS +FL SA    T    IILLH FWG+VFFD CE  
 Sbjct: 125    FGIISGVFSVINILADALGPGVVGHIHGDSPPYYFLTS AFLTAAIILLHTFWGVVFFDACER 184

Query: 170    K--WGILLIALTHLLVSAQTFISSYYGINLMAFIILVV--GTWAFIAAGGSCRS 219  
 +    W + L+    +HLL S    TF++ +Y    +L+    + V    G WAFI AGGS RS  
 Sbjct: 185    RRYWALGLVVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRS 238

□ >gi|22203751|ref|NP\_666216.1|    L    anterior pharynx defective 1A homolog; anterior 1A homolog (C. elegans) [Mus musculus]  
 gi|15341753|gb|AAH12406.1|    L    Anterior pharynx defective 1A homolog [Mus musculus]  
 gi|34786036|gb|AAH57865.1|    L    Anterior pharynx defective 1A homolog [Mus musculus]  
 Length = 247

Score = 172 bits (436), Expect = 5e-42  
 Identities = 124/234 (52%), Positives = 159/234 (67%), Gaps = 18/234 (7%)

Query: 4    VFFGCAFIAGP--MYVFTIAEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGC F+AFGP    +++ T+A +PLR+I L+AGAF    LVSLL++S+ WF+    D D  
 Sbjct: 5    VFFGCTFVAFGPAFSLFLITVAGDPLRVIIILVAGAFFWLVSSLASVVWFILVHVTDRSD 64

Query: 60    GPTQKYLLIFGAWS--WIQEMF--AYYKLLKMS-EGLKSINPGETAP-SMRLM-YVSGLG 112  
 Q    LLIFGA    +QE+F    AYYKLLK + EGL S++    +P S+R M YVSGL  
 Sbjct: 65    ARLQYGLLIFGAAVSVLQEVFRFAYYKLLKADEGLASLSEDGRSPISIRQMAVSGLS 124

Query: 113    FGIMSGVFSMT--LSDSLGPGTVGIHGDSQFFLYSAG-TLVIILLHVFWGIVFFDGCEM 169  
 FGI+SGVFS+    L+D+LGPG    VGIHGDS +FL SA    T    IILLH FWG+VFFD CE  
 Sbjct: 125    FGIISGVFSVINILADALGPGVVGHIHGDSPPYYFLTS AFLTAAIILLHTFWGVVFFDACER 184

Query: 170    K--WGILLIALTHLLVSAQTFISSYYGINLMAFIILVV--GTWAFIAAGGSCRS 219  
 +    W + L+    +HLL S    TF++ +Y    +L+    + V    G WAFI AGGS RS  
 Sbjct: 185    RRYWALGLVVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRS 238

□ >gi|14250557|gb|AAH08732.1|    L    APH-1A protein [Homo sapiens]  
 gi|14550502|gb|AAH09501.1|    L    APH-1A protein [Homo sapiens]  
 gi|17389295|gb|AAH17699.1|    L    APH-1A protein [Homo sapiens]  
 gi|22761292|gb|BAC11529.1|    L    unnamed protein product [Homo sapiens]  
 gi|25989508|gb|AAM61955.1|    L    presenilin stabilization factor a [Homo sapiens]  
 gi|37183020|gb|AAQ89310.1|    L    GAAV579 [Homo sapiens]  
 Length = 247

Score = 172 bits (436), Expect = 6e-42  
 Identities = 124/234 (52%), Positives = 159/234 (67%), Gaps = 18/234 (7%)

Query: 4    VFFGCAFIAGP--MYVFTIAEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGC F+AFGP    +++ T+A +PLR+I L+AGAF    LVSLL++S+ WF+    D D

Sbjct: 5 VFFGCTFVAFGPAFALFLITVAGDPLRVIILVAGAFFWLVSLLASVWWFILVHVTDRSD 64

Query: 60 GPTQKYLLIFGAWS--WIQEMF--AYYKLLKMS-EGLKSINPGETAP-SMRLM-YVSGLG 112  
 Q LLIFGA +QE+F AYYKLLK + EGL S++ +P S+R M YVSGL

Sbjct: 65 ARLQYGLLIFGAAVSLLQEVFRFAYYKLLKADEGLASLSEDGRSPISIRQMAYVSGLS 124

Query: 113 FGIMSGVFSMT--LSDSLGPGTVGIHGDSQPFLYSAG-TLVIILLHVFWGIVFFDGCEM 169  
 FGI+SGVFS+ L+D+LGPG VGIHGDS +FL SA T IILLH FWG+VFFD CE

Sbjct: 125 FGIIISGVFSVINILADALGPGVVGHIHGDSPYFLTSALTAIIILLHTFWGVVFFDACER 184

Query: 170 K--WGILLIALTHLLVSAQTFIISYYGINLMAFIILVV--GTWAFIAAGGSCRS 219  
 + W + L+ +HLL S TF++ +Y +L+ + V G WAFI AGGS RS

Sbjct: 185 RRYWALGLVVGSLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRS 238

[>gi|41056229|ref|NP\_956409.1| L anterior pharynx defective 1B [Danio rerio]  
 gi|37077309|sp|Q8JHE9|AP1B\_BRARE Gamma-secretase subunit Aph-1b (Anterior-pharynx  
 1b)  
 gi|22001127|gb|AAM88325.1| L Aph-1 protein [Danio rerio]  
 gi|37682171|gb|AAQ98012.1| L anterior pharynx defective 1B-like [Danio rerio]  
 gi|47939453|gb|AAH71492.1| L Unknown (protein for MGC:86848) [Danio rerio]  
 Length = 258

Score = 171 bits (433), Expect = 1e-41  
 Identities = 125/235 (53%), Positives = 164/235 (69%), Gaps = 20/235 (8%)

Query: 4 VFFGCAFIAGPMM--MYVFTIAEPLRIIFLIAGAF--NLVSLLISSLWFMARVTIDNKD 59  
 VFFGC FIAFGP +FTIA +PLR+IFLIAGAF + LL S +WF+ V I NK+  
 Sbjct: 5 VFFGCTFIAFGPAIALFMFTIARDPLRVIIFLIAGAFFWLVSLLLSSLVWFIT-VQISNKN 63

Query: 60 GPTQKY-LLIFGA--WSWIQEMF--AYYKLLKMS-EGLKSINPGETAP-SMR-LMYVSGL 111  
 TQ+ LLIFG +QE F YY+LLK + EGL +++ +T P SMR L YVSGL  
 Sbjct: 64 SATQQQRGLLIFGVVLSVLLQEAFRYGYRLLKKANEGLLALSQEDTMPISMRQLAYVSGL 123

Query: 112 FGIMSGVFSMT--LSDSLGPGTVGIHGDSQPFLYSAG-TLVIILLHVFWGIVFFDGCE 168  
 GFG MSG FS+ LSDSLGPGTVGIHG+S +F+ SA TL IILLH+FWG+VFF+ CE  
 Sbjct: 124 GFGFMSGAFSVNILSDSLGPGTVGIHGESQHYFISSAFMTLAIILLHMFWGVVFFEACE 183

Query: 169 MK--WGILLIALTHLLVSAQTFIISYYGINLMAFIIL-VVGTWAFIAAGGSCRS 219  
 + W + +HL+VS TF++ +Y +L+ +IIL V+ WA++ AGGS R+  
 Sbjct: 184 RQRWWALGAVVASHLVVSLTFVNPHYQGSLIPTYIILSVMWAYLCAGGSLRN 238

[>gi|34864287|ref|XP\_343418.1| L similar to RIKEN cDNA 0610008A10 [Rattus norvegicus]  
 Length = 216

Score = 171 bits (432), Expect = 1e-41  
 Identities = 135/249 (54%), Positives = 156/249 (62%), Gaps = 52/249 (20%)

Query: 4 VFFGCAFIAGPMM--YVFTIAEPLRIIFLIAGAFN-LVSLLISSL-WFMARVTIDNKD 59  
 VFFGCAFIAGP + YVFTIA +PLR+IFLIAGAF LVSLISSL WF+ RV DN+D  
 Sbjct: 5 VFFGCAFIAGPALS LYVFTIATDPLRVIIFLIAGAFFWLVSLLLSSVFWFLVRVITDNRD 64

Query: 60 GPTQKYLLIFGAWS--SWIQEMF--AYYKLLKMS-EGLKSINPGETAPSMRLMYVSGLGFG 114  
 GP Q YLLIFG IQE+F AYY+LLK + EGLKSINP ETAPSMRL+  
 Sbjct: 65 GPVQNYLLIFGVLLSVCIQELFRLAYYRLLKKANEGLKSINPEETAPSMRL----- 116

Query: 115 IMSGVFSMTLSDSLPGTVGIHGDSPQFFLYSAGTLVIIILLHVFWGIVFFDGCEM-KWGI 173

Y+ TLVII+LHVFWGIVFFDGCE KW I

Sbjct: 117 -----AYAFMTLVIIMLHVFWGIVFFDGCEKNKWIYI 147

Query: 174 -LLIALTHLLVSAQTFISSLYYGINLM-AFIILVV-GTWAFIAAGGSCRS--XXXXXXXXX 228

L + LTHLLVS QT +S +Y +NL+ A+II+V+ G WAF AGGS RS

Sbjct: 148 LLTVLLTHLLVSTQTLSPHYEVNLVTAYIIMVLMGIWAFCVAGGSRRSLKLCLLCQDKD 207

Query: 229 XXXYNQRSR 237

YNQRSR

Sbjct: 208 FLLYNQRSR 216

 >gi|26347159|dbj|BAC37228.1|  unnamed protein product [Mus musculus]  
Length = 152

Score = 120 bits (301), Expect = 2e-26

Identities = 77/143 (53%), Positives = 97/143 (67%), Gaps = 9/143 (6%)

Query: 86 KMSEGLKSINPGETAP-SMRLM-YVSGLGFGIMSGVFSMT--LSDSLGPGTVGIHGDSPQ 141

K EGL S++ +P S+R M YVSGL FGI+SGVFS+ L+D+LGPG VGIHGDSP

Sbjct: 1 KADEGLASLSEDGRSPISIRQMAVSGLSFGIISGVFSVINILADALGPGVVGIHGDSPY 60

Query: 142 FFLYSAG-TLVIILLHVFWGIVFFDGCEMK--WGILLIALTHLLVSAQTFISSLYYGINLM 198

+FL SA T IILLH FWG+VFFD CE + W + L+ +HLL S TF++ +Y +L+

Sbjct: 61 YFLTSAFLTAIIILLHTFWGVVFFDACCERRRYWALGLVVGSHLLTGLTFLNPWYEASLL 120

Query: 199 AFIILVV--GTWAFIAAGGSCRS 219

+ V G WAFI AGGS RS

Sbjct: 121 PIYAVTVSMGLWAFITAGGSLRS 143

 >gi|31233667|ref|XP\_318923.1| ENSANGP00000015809 [Anopheles gambiae]  
gi|30174614|gb|EAA14158.2| ENSANGP00000015809 [Anopheles gambiae str. PEST]  
Length = 247

Score = 117 bits (294), Expect = 2e-25

Identities = 97/237 (40%), Positives = 140/237 (59%), Gaps = 22/237 (9%)

Query: 1 MTMV-FFGCAFIAFGP--MMYVFTIAEPLRIIFLIAGAFN-LVSLLISSLWFMARVTID 56

MT+V FFGC+F+AFGP M+ TIA +P+RII LIA +F LVSLL+SS ++A +

Sbjct: 7 MTVVEFFGCSFLAFGPPVAMFALTIAHDPIRIIILIAASFFWLVSLLSSTVWLAFHPVT 66

Query: 57 NKDGPTQKYLLIFGAWSWIQEMFAY--YKLLKMSE-GLKSINPGETAPSMR--LMYVSGL 111

+K + LI + + + F Y YK+L+ +E GL+ + R L Y SGL

Sbjct: 67 SK---VTGLICSVFIQVCKRFRYLMYKVLRKTESGLQEVTDIVRIADYRHILSYASGL 122

Query: 112 GFGIMSGVFSMT--LSDSLGPGTVGIHGDSPQFFLYSAG-TLVIILLHVFWGIVFFDGCE 168

GFGI+SG FS+ L+DS+GP TVG+ S F L SA +L +ILLH FW ++FF+ C+

Sbjct: 123 GFGIISGAFSLVNILADSGPATVGLKAASDIFMLISAAQSLAMILLHTFWSVIFFNACD 182

Query: 169 MK--WGILLIALTHLLVSAQTFI--SSYYGINLMA--FIILVVGTVAFIAAGGSCRS 219

+K + I + +HL VS T + S Y + L+ ++ + G AF AGG+ S

Sbjct: 183 VKNYYHIGYVVASHLFVSCMTLLNASGLYAVTLLISYTMVCITGAIASFQVAGGTVAS 239